



A-688A.ST25.txt
SEQUENCE LISTING

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LACEY, DAVID LEE
BOONE, THOMAS CHARLES

<120> INTEGRIN/ADHESION ANTAGONISTS

<130> A-688A

<140> 09/840,277

<141> 2001-04-23

<150> 60/198,919

<151> 2000-04-21

<150> 60/201,394

<151> 2000-05-03

<160> 135

<170> PatentIn version 3.1

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ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
20 25 30	
atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
35 40 45	
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
50 55 60	
gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg	240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
65 70 75 80	
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
85 90 95	
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc	336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
100 105 110	
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag	384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
115 120 125	

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gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc      432
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
130                               135                               140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                               150                               155                               160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165                               170                               175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180                               185                               190

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195                               200                               205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
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Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
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Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35      40      45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
50      55      60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65      70      75      80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
85      90      95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
100     105     110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
115     120     125

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A-688A.ST25.txt

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 130 135 140
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 145 150 155 160
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 165 170 175
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 180 185 190
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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Thr Glu Glu

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<400> 79

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 1 5 10

<210> 80
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Selectin antagonist peptide

<400> 80

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
 1 5 10

<210> 81
 <211> 12
 <212> PRT
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<220>
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<400> 81

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
 1 5 10

<210> 82
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 82

Cys Gln Asn Arg Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Asn Glu
 1 5 10 15

<210> 83
 <211> 17
 <212> PRT
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<220>
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<400> 83

Ala Glu Asn Trp Ala Asp Asn Glu Pro Asn Asn Lys Arg Asn Asn Glu
 1 5 10 15

Asp

<210> 84
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Selectin antagonist peptide

<400> 84

Arg	Lys	Asn	Asn	Lys	Thr	Trp	Thr	Trp	Val	Gly	Thr	Lys	Lys	Ala	Leu
1				5					10					15	

Thr Asn Glu

<210> 85

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Selectin antagonist peptide

<400> 85

Lys	Lys	Ala	Leu	Thr	Asn	Glu	Ala	Glu	Asn	Trp	Ala	Asp
1				5					10			

<210> 86

<211> 16

<212> PRT

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<220>

<223> Selectin antagonist peptide

<220>

<221> misc_feature

<222> (3 and)..(15)

<223> Xaa is any amino acid residue

<400> 86

Cys	Gln	Xaa	Arg	Tyr	Thr	Asp	Leu	Val	Ala	Ile	Gln	Asn	Lys	Xaa	Glu
1				5					10					15	

<210> 87

<211> 17

<212> PRT

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<220>

<221> misc_feature

<222> (13 and)..(15)

<223> Xaa is any amino acid residue

<400> 87

Ala	Glu	Asn	Trp	Ala	Asp	Gly	Glu	Pro	Asn	Asn	Lys	Xaa	Asn	Xaa	Glu
1				5					10					15	

Asp

<210> 88
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<220>
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<400> 88

Ser Ser Gln Asn Trp Asp Met Glu Ala Gly Val Glu Asp Leu Thr Ala
 1 5 10 15

Ala Met Leu Gly Leu Leu Ser Thr Ile His Ser Ser Ser Arg
 20 25 30

<210> 89
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Vinculin binding peptide

<400> 89

Ser Ser Pro Ser Leu Tyr Thr Gln Phe Leu Val Asn Tyr Glu Ser Ala
 1 5 10 15

Ala Thr Arg Ile Gln Asp Leu Leu Ile Ala Ser Arg Pro Ser Arg
 20 25 30

<210> 90
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Vinculin binding peptide

<400> 90

Ser Ser Thr Gly Trp Val Asp Leu Leu Gly Ala Leu Gln Arg Ala Ala
 1 5 10 15

Asp Ala Thr Arg Thr Ser Ile Pro Pro Ser Leu Gln Asn Ser Arg
 20 25 30

<210> 91
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Vinculin binding peptide

<400> 91

Asp Val Tyr Thr Lys Lys Glu Leu Ile Glu Cys Ala Arg Arg Val Ser
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Glu Lys

<210> 92
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Vinculin binding peptide

<400> 92

Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Gly Val Ser
 1 5 10 15

Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg
 20 25

<210> 93
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Vinculin binding peptide

<400> 93

Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Arg Val Ser
 1 5 10 15

Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg
 20 25

<210> 94
 <211> 30
 <212> PRT
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<220>
 <223> Vinculin binding peptide

<400> 94

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Met Lys Glu Ala Ser Asn Val Phe Pro Ser Arg Arg Ser Arg
 20 25 30

<210> 95
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Laminin related peptide |

<400> 95

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Arg Glu Asp Val Glu Ile Leu Asp Val Tyr Ile Gly Ser Arg Pro Asp
1 5 10 15

Ser Gly Arg

<210> 96
<211> 19
<212> PRT
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<220>
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<400> 96

Tyr Ile Gly Ser Arg Arg Glu Asp Val Glu Ile Leu Asp Val Pro Asp
1 5 10 15

Ser Gly Arg

<210> 97
<211> 44
<212> DNA
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44

<210> 98
<211> 44
<212> DNA
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<400> 98
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44

<210> 99
<211> 44
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<213> Artificial Sequence

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44

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<211> 51
<212> DNA
<213> Artificial Sequence

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<223> Used to form echistatin template for PCR

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51

<210> 101

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Used to form echistatin template for PCR

<400> 101

ttcaagaact tacagtttct gcag

24

<210> 102

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Used to form echistatin template for PCR

<400> 102

cgtccatgtc gtcacctcta gctc

24

<210> 103

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Used to form echistatin template for PCR

<400> 103

gtgtgggttt ctcgggcagt caca

24

<210> 104

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

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ccgggtaaag gtggaggtgg tggatgaatgt gaatctgggc catgctgc

48

<210> 105

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 105

ccgggtaaag gtggaggtgg tggatgaatgt gaatctgggc catgctgc

48

<210> 106

<211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 106
 aacataagta cctgtaggat cg

22

<210> 107
 <211> 49
 <212> DNA
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<220>
 <223> PCR primer

<400> 107
 gcagcatgga ccagattcac attcaccacc acctccacct ttacccgga

49

<210> 108
 <211> 859
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Echistatin Fc-peptide

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 <223>

<220>
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 <223> NdeI site

<220>
 <221> misc_feature
 <222> (854)..(854)
 <223> BamHI site

<400> 108
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 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
 1 5 10 15

48

ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc
 Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

96

ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

144

agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60

192

gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

240

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65	70	75	
acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg			288
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu			
80	85	90	95
aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc			336
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	100	105	110
ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca			384
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	115	120	125
cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag			432
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln			
	130	135	140
gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc			480
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
	145	150	155
gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg			528
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
	160	165	170
cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc			576
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
	180	185	190
acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc			624
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
	195	200	205
gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc			672
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
	210	215	220
ctg tct ccg ggt aaa ggt gga ggt ggt ggt gaa tgt gaa tct ggt cca			720
Leu Ser Pro Gly Lys Gly Gly Gly Gly Gly Glu Cys Glu Ser Gly Pro			
	225	230	235
tgc tgc aga aac tgt aag ttc ttg aag gaa ggt acc atc tgt aag aga			768
Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu Gly Thr Ile Cys Lys Arg			
	240	245	250
gct aga ggt gac gac atg gac gac tac tgt aac ggt aag acc tgt gac			816
Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys Asn Gly Lys Thr Cys Asp			
	260	265	270
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Cys Pro Arg Asn Pro His Lys Gly Pro Ala Thr			
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<210> 109
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 <212> PRT
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 <223> NdeI site

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<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> NdeI site

<220>
 <221> misc_feature
 <222> (854)..(854)
 <223> BamHI site

<400> 109

Met	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	1	5	10	15
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Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	35	40	45	
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	50	55	60	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	65	70	75	80
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	85	90	95	
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	100	105	110	
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	115	120	125	
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	130	135	140	
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	145	150	155	160
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	165	170	175	
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	180	185	190	
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	195	200	205	
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	210	215	220	
Ser	Pro	Gly	Lys	Gly	Gly	Gly	Gly	Gly	Glu	Cys	Glu	Ser	Gly	Pro	Cys	225	230	235	240
Cys	Arg	Asn	Cys	Lys	Phe	Leu	Lys	Glu	Gly	Thr	Ile	Cys	Lys	Arg	Ala				

Arg Gly Asp Asp Met Asp Asp Tyr Cys Asn Gly Lys Thr Cys Asp Cys
 260 265 270

Pro Arg Asn Pro His Lys Gly Pro Ala Thr
 275 280

<210> 110
 <211> 140
 <212> DNA
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 <223> pAMG21

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 <223> AatII site

<220>
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 <222> (140)..(140)
 <223> claI site

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 ggcggtgata ctgagcacat 140

<210> 111
 <211> 55
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pAMG21

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 <223> ClaI site

<220>
 <221> misc_feature
 <222> (55)..(55)
 <223> KpnI site

<400> 111
 cgatttgatt ctagaaggag gaataacata tgggtaacgc gttggaattc ggtac 55

<210> 112
 <211> 1546
 <212> DNA
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<220>

<223> pAMG21

<220>

<221> misc_feature

<222> (1)..(1)

<223> AatII sticky end

<220>

<221> misc_feature

<222> (1546)..(1546)

<223> SacII sticky end

<400> 112

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ctcctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccgga      180
gggtggcggg caggacgccc gccataaact gccaggcatc aaattaagca gaaggccatc      240
ctgacggatg gcctttttgc gtttctacaa actcttttgt ttatttttct aaatacatc      300
aaatatggac gtcgtactta acttttaaag tatgggcaat caattgctcc tgttaaaatt      360
gcttttagaa tactttggca gcggtttgtt gtattgagtt tcatttgccg attggttaaa      420
tggaagtgta ccgtgcgctt actacagcct aatatttttg aaatatccca agagcttttt      480
ccttcgcatg cccacgctaa acattctttt tctcttttgg ttaaactcgtt gtttgattta      540
ttatttgcta tatttatattt tcgataatta tcaactagag aaggaacaat taatgggatg      600
ttcatacacg catgtaaaaa taaactatct atatagttgt ctttctctga atgtgcaaaa      660
ctaagcattc cgaagccatt attagcagta tgaataggga aactaaacc agtgataaga      720
cctgatgatt tcgcttcttt aattacattt ggagattttt tatttacagc attgttttca      780
aatatattcc aattaatcgg tgaatgattg gagttagaat aatctactat aggatcatat      840
tttattaaat tagcgtcatc ataattttgc ctccattttt tagggtaatt atccagaatt      900
gaaatatcag atttaaccat agaatgagga taaatgatcg cgagtaaata atattcacia      960
tgtaccattt tagtcatatc agataagcat tgattaatat cattattgct tctacaggct     1020
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ttatccttac ctattgtttg tcgcaagttt tgcgtgttat atatcattaa aacggtaata     1140
gattgacatt tgattctaataaattggatt tttgtcacac tattatatcg cttgaaatac     1200
aattgtttta cataagtacc tgtaggatcg tacaggttta cgcaagaaaa tggtttgttta     1260
tagtcgatta atcgatttga ttctagattt gttttaacta attaaaggag gaataacata     1320
tggttaacgc gttggaattc gagctcacta gtgtcgacct gcagggtacc atggaagctt     1380
actcgaggat ccgcggaaag aagaagaaga agaagaaagc ccgaaaggaa gctgagttgg     1440
ctgctgccac cgctgagcaa taactagcat aaccctttgg gcctctaaa cgggtcttga     1500
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<210> 113
 <211> 872
 <212> DNA
 <213> Artificial Sequence

<220>
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 gataatatat gagcacaaaa aagaaaccat taacacaaga gcagcttgag gacgcacgtc 180
 gccttaaagc aatttatgaa aaaaagaaaa atgaacttgg cttatcccag gaatctgtcg 240
 cagacaagat ggggatgggg cagtcaggcg ttggtgcttt atttaatggc atcaatgcat 300
 taaatgctta taacgccgca ttgcttacia aaattctcaa agttagcgtt gaagaattta 360
 geccttcaat cgccagagaa tctacgagat gtatgaagcg gttagtatgc agccgtcact 420
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 gcttagaacc ttaccaaaag gtgatgccga gagatgggta agcacaacca aaaaagccag 540
 tgattctgca ttctggcttg aggttgaagg taattccatg accgcacca caggctccaa 600
 gccaaagcttt cctgacggaa tgtaattct cgttgaccct gagcaggctg ttgagccagg 660
 tgatttctgc atagccagac ttgggggtga tgagtttacc ttcaagaaac tgatcaggga 720
 tagcggtcag gtgtttttac aaccactaaa cccacagtac ccaatgatcc catgcaatga 780
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 atagactagt ggatccacta gtgtttctgc cc 872

<210> 114
 <211> 1197
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<220>
 <223> GM221

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 gcgtggcaca acaactggcg ggcaaacagt cgctcctgat tggcgttgcc acctccagtc 300
 tggccctgca cgcgccgtcg caaattgtcg cggcgattaa atctcgcgcc gatcaactgg 360
 gtgccagcgt ggtggtgtcg atggtagaac gaagcggcgt cgaagcctgt aaagcggcgg 420
 tgcacaatct tctcgcgcaa cgcgtcagtg ggctgatcat taactatccg ctggatgacc 480
 aggatgccat tgctgtggaa gctgcctgca ctaatgttcc ggcgttatatt cttgatgtct 540

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ctgaccagac acccatcaac agtattattt tctcccatga agacggtacg cgactgggcg      600
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ctgtctcggc gcgtctgcgt ctggctggct ggcataaata tctactcgc aatcaaattc      720
agccgatagc ggaacgggaa ggcgactgga gtgccatgtc cggttttcaa caaacatgc      780
aaatgctgaa tgagggcatc gttccactg cgatgctggt tgccaacgat cagatggcgc      840
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tgggatacga cgataccgaa gacagctcat gttatatccc gccgttaacc accatcaaac      960
aggattttcg cctgctgggg caaacccagc tggaccgctt gctgcaactc tctcagggcc     1020
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cgcccaatac gcaaaccgcc tctccccgcg cgttggccga ttcattaatg cagctggcac     1140
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<210> 115
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
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 <400> 115

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 1 5 10

<210> 116
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
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 <400> 116

Met Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
 1 5 10 15

<210> 117
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Laminin related peptide
 <400> 117

Met Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
 1 5 10 15

Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
 20 25

<210> 118
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Laminin related peptide

<400> 118

Met Ile Pro Cys Asn Asn Lys Gly Ala His Ser Val Gly Leu Met Trp
 1 5 10 15

Trp Met Leu Ala Arg Gly Gly Gly Gly Gly
 20 25

<210> 119
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Laminin related peptide

<400> 119

Met Tyr Ile Gly Ser Arg Arg Glu Asp Val Glu Ile Leu Asp Val Pro
 1 5 10 15

Asp Ser Gly Arg Gly Gly Gly Gly Gly
 20 25

<210> 120
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Laminin related peptide

<400> 120

Met Arg Gly Asp Arg Gly Asp Tyr Ile Gly Ser Arg Arg Gly Asp Gly
 1 5 10 15

Gly Gly Gly Gly
 20

<210> 121
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encoding Laminin related peptide, for PCR reaction to yield in-fr
 ame fusion to Fc

<400> 121
 gaataacata tgtacatcgg ttctcgtggt ggaggcggtg gggacaaa

48

<210> 122
 <211> 81
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Encoding Laminin related peptide, for PCR reaction to yield in-frame fusion to Fc

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 gaataacata tgtacatcgg ttctcggttat attggctccc gctacattgg tagccgtgac 60
 aaaactcaca catgtccacc t 81

<210> 123
 <211> 111
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<220>
 <223> Encoding Laminin related peptide, for PCR reaction to yield in-frame fusion to Fc

<400> 123
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<220>
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<400> 124
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<220>
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<210> 127
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ame fusion to Fc

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<210> 128
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<400> 128

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1 5 10

<210> 129
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<220>
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<400> 129

Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
1 5 10 15

<210> 130
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<220>
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<400> 130

Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr
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Ile Gly Ser Arg
20

<210> 131
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<212> PRT
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<220>
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<400> 131

Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr
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Ile Gly Ser Arg Tyr Ile Gly Ser Arg
 20 25

<210> 132
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<400> 132

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Met Leu Ala Arg
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 <212> PRT
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<400> 133

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Ser Gly Arg

<210> 134
 <211> 14
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<400> 134

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<210> 135
 <211> 25

<212> PRT

<213> Artificial Sequence

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<223> Laminin related peptide

<400> 135

Tyr	Ile	Gly	Ser	Arg	Tyr	Ile	Gly	Ser	Arg	Tyr	Ile	Gly	Ser	Arg	Tyr
1				5				10						15	

Ile	Gly	Ser	Arg	Tyr	Ile	Gly	Ser	Arg
			20					25